IN THE SPECIFICATION:

Please amend the specification as shown:

Please delete the paragraph on page 6, line 6, and replace it with the following paragraph:

Fig. 1 is a schematic of the genetic map of NDV genomic RNA **(SEQ ID NOS 1 and 2)**.

Please delete the paragraph on page 6, lines 7-9, and replace it with the following paragraph:

Fig. 2 is the complete map of the genome of NDV strain Beaudette C, wherein the nucleotide sequence of the NP region is available from the GenBank database with the accession number AF064091 **(SEQ ID NO: 3 is shown at the top, SEQ ID NOS 4-8, and 2 are shown on the left side, respectively in order of appearance, SEQ ID NO: 1 is shown on the right side, and SEQ ID NO: 9 is shown on the bottom of the figure)**.

Please delete the paragraph on page 6, lines 10-12, and replace it with the following paragraph:

Fig. 3 shows the nucleotide sequences of the leader **(SEQ ID NO: 12)** and trailer **(SEQ ID NO: 13)** regions of NDV strain B1 in comparisons with corresponding sequences from NDV strain Beaudette C **(SEQ ID NOS 11 and 9 are the leader and trailer respectively)** and NDV strain D26 **(SEQ ID NO: 10)**.

Please delete the paragraph on page 6, line 27, and replace it with the following paragraph:

Fig. 12. Recombinant NDVs showing location of cleavage site mutations (SEQ ID NOS 14 and 15).

Please delete the paragraph on page 8, line 18, to page 9, line 5, and replace it with the following paragraph:

NDV strain Beaudette C was received from the National Veterinary Services Laboratory at Ames, Iowa, U.S.A. and was propagated in the allantoic cavity of embryonated chicken eggs. The virus was purified as described previously (Kingsbury, *J. Mol. Biol.*, vol. 18, pp. 195-203, 1966). The virion RNA was extracted using proteinase K and TRIzol reagent (Life Technologies). The NP gene, intergenic regions and 5' trailer region were obtained by RT-PCR of the virion RNA. The cDNAs were synthesized using Superscript II reverse transcriptase (Life Technologies). The cDNA corresponding to the NP gene was synthesized using a positive-sense primer, 5' GAAGGTGTGAATCTCGAGTGCG (SEQ ID NO: 16), complementary to the established sequence at the start of the NP gene. This primer and a negative-sense primer corresponding to the 3' end of the P gene, 5' GCTCGTCGATCTCCGCATCTGT (SEQ ID NO: 17), were used in PCR with high fidelity *Pfu* DNA polymerase (Stratagene). The PCR product was cloned and sequenced by the dideoxynucleotide chain termination method. For obtaining cDNAs corresponding to the intergenic regions, the positive-sense oligonucleotide primer was derived from a sequence upstream of the respective gene junction. Likewise, the negative-sense primer was derived from a sequence downstream of that gene junction. The PCR product was cloned and sequenced by the dideoxynucleotide chain termination method.

Please delete the paragraph on page 9, lines 6-18, and replace it with the following paragraph:

The 5' trailer region was cloned using the 5' RACE method (Dorit, in *Current Protocols in Molecular Biology*, vol. 2, pp. 15.6.1-15.6.10, 1995). Briefly, a positive-sense primer, 5' CACTAAGGACATACTTGAAGC **(SEQ ID NO: 18)**, complemenatry to the downstream end of the L gene was extended with reverse transcriptase and the resulting cDNAs were tailed with dCTP, and separately with dGTP, using terminal deoxynucleotidy transferase. The cDNAs were then amplified by PCR by using the L gene-specific primer described above and either oligo(dG) primer for reactions tailed with dC, or oligo(dC) primer for reactions tailed with dG. The PCR products were then cloned and sequenced by the dideoxynucleotide chain termination method. Tailing reactions with C and G residues assured unambiguous determination of the 5' terminal nucleotide. To sequence the 3' leader region, virion RNA was ligated to a synthetic RNA, and cDNA was made using RT-PCR. The PCR product was cloned and sequenced by the dideoxynucleotide chain termination method.